

Please replace the paragraph starting with “This application claims priority...” at page 1, line 5, with the following amended paragraph:

Please amend Table 2 on page 9 as follows:

### Comparison between a NOV1 polypeptide and thymosin beta-10 from human

Please amend Table 3 on page 9 as follows:

### Multiple Sequence alignment of a NOV1 polypeptide and the thymosin beta family

(Black outlined amino acids indicate potential regions of conserved sequence; grayed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs. Sequences may be referenced by the SWISSPROT or TREMBL ID.)

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**Table 4.**  
**PFAM alignment of a NOV1 polypeptide to the consensus sequence of the thymosin beta family**

Please amend Table 6 beginning on page 13 as follows:

NOV2: 361 TYNAVCRRCPWALSACEAGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420  
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      TFNLVYLESDRDLGASTQESQFLKIDTIAADESFTCADLGVRRLKLNTEVRSVGPLSKRG
Sbjct: 121 TFNLVYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180

NOV2 : 181 FYLAFQDIGACLAAILSLRIYYKKCPAMVRNLAASFSEAVTGADSSSLVEVRGQCVRHSEER 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 FYLAFQDIGACLAAILSLRIYYKKCPAMVRNLAASFSEAVTGADSSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI
Sbjct: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNACRRCPWALSRCACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361 TYNACRRCPWALSRCACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKAVTTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      DKEMQSYSTLKAVTTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT
Sbjct: 481 DKEMQSYSTLKAVTTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTLITGLVVLVLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541 RTIVWICLTLITGLVVLVLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPQR 660
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPQR 660

NOV2 : 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTGRRLAMIVTEYMENG 720
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTGRRLAMIVTEYMENG 720

NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780

NOV2 : 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840

NOV2 : 841 NMTNRDVISSVEEGYRLPAPMGC PHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMGC PHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900

NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960

NOV2 : 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)

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Please amend the paragraph beginning at line 4 in Table 7 on page 16 as follows:

Table 7 shows multiple sequence alignment of the NOV2 ephrim type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2 , with similar proteins. The

various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please amend the paragraph beginning at line 5 in Table 9 on page 20 as follows:

Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family:  
AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please amend Table 9. continued on page 21 as follows:

**TABLE 9. continued TABLE 9A.**

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>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein
FLRT1 [Homo
      sapiens]
      Length = 674

      Score = 1365 bits (3494), Expect = 0.0
      Identities = 673/674 (99%), Positives = 674/674 (99%)

NOV3:   1   MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60
      |||
Sbjct:  1   MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60

NOV3:   61   DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120
      |||
Sbjct:  61   DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120

NOV3:   121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNSVSTVSIEEDAFADSKQLK 180
      |||
Sbjct:  121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNSVSTVSIEEDAFADSKQLK 180

NOV3:   181  LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240
      |||
Sbjct:  181  LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240

NOV3:   241  DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300
      |||
Sbjct:  241  DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300

NOV3:   301  LSNNNLTTLPRGLFDDLG NLAQLLRNNPWF CGCNLMWLRDWWKARA AVNVVRGLMCQGP 360
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Sbjct: 301 LSNNNLTTLPRGLFDDLGNLAQLLLRNPNWFCGCNLMWLRDWMKARAAVVNVRLMCQGP 360
NOV3: 361 EKVRGMAIKDITSEMDECFTGPGGGVANAAAKTTASNHASATTPQGSFRTLKAKRPGLR 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361 EKVRGMAIKDITSEMDECFTGPGGGVANAAAKTTASNHASATTPQGSFRTLKAKRPGLR 420
NOV3: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480
NOV3: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAYVADETPVCAKAETADSYGPTTTLN 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAYVADETPVCAKAETADSYGPTTTLN 540
NOV3: 541 QEQNAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGRKDDY 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||+|||
Sbjct: 541 QEQNAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGRKDDY 600
NOV3: 601 MESGTKKDNSILEIRGPGQLMPLINPYRAKEEYVVHTIFPSNGSSLCKATHHTIGYGTTRG 660
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601 MESGTKKDNSILEIRGPGQLMPLINPYRAKEEYVVHTIFPSNGSSLCKATHHTIGYGTTRG 660
NOV3: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:7)
      ||||||||||||
Sbjct: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:60)

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Please amend the paragraph beginning at line 6 in Table 10 on page 22 as follows:

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please insert sequence listing pages 1-47 at the end of the specification.